

PATENT APPLICATION

03C0
Box/seq.
#5

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Yoshinaga et al.

Serial No.: 09/728,420

Filed: November 28, 2000

For: Novel Polypeptides Involved in Immune Response

Docket No.: A-579C

RESPONSE TO NOTICE TO COMPLY
AND
ATTORNEY'S STATEMENT PURSUANT TO 37 CFR § 1.821

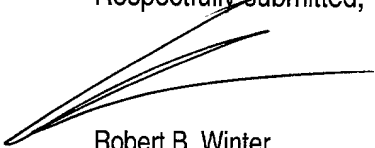
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures dated June 7, 2001.

I hereby state that the substitute paper copy and computer readable form (CRF) of the "Sequence Listing" submitted herewith for the above-mentioned patent application are the same, and contain no new matter.

Respectfully submitted,


Robert B. Winter
Attorney/Agent for Applicant(s)
Registration No.: 34,458
Phone: (805) 447-2425
Date: *JUNE 27, 2001*

Please send all future correspondence to:

U.S. Patent Operations/RBW
Dept. 4300, M/S 27-4-A
AMGEN INC.
One Amgen Center Drive
Thousand Oaks, California 91320-1799

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231, on the date appearing below.

June 28, 2001

Date

D. Dillan

Signature

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Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
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Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
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Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
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Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
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Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

<210> 13

<211> 267

<212> PRT

<213> Homo sapiens

<400> 13

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<213> Artificial sequence

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<223> Synthetic

<400> 15

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Ser Met Gly Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys
35 40 45
Val Leu Val Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr
50 55 60
Thr Cys Ser Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn
65 70 75 80
Ser Leu Asp Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val
85 90 95
Ser Leu Arg Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly
100 105 110
Lys Lys Leu Ala Val Leu Val Ile Arg Arg Ser Tyr Gly
115 120 125

<210> 16

<211> 1294

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> (1)..(199)

<220>

<221> CDS

<222> (200)..(1105)

<400> 16

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cgctccgcggg agcgcagtta gagccgatct cccgcgcccc gaggttgctc ctctccgagg 120

0923420.0001

[illegible]

Ile	Gly	Glu	Arg	Asp	Lys	Ile	Thr	Glu	Asn	Pro	Val	Ser	Thr	Gly	Glu		
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aaa	aac	gcg	gcc	acg	tgg	agc	atc	ctg	gct	gtc	ctg	tgc	ctg	ctt	gtg		1000
Lys	Asn	Ala	Ala	Thr	Trp	Ser	Ile	Leu	Ala	Val	Leu	Cys	Leu	Leu	Val		
			255					260					265				
gtc	gtg	gcg	gtg	gcc	ata	ggc	tgg	gtg	tgc	agg	gac	cga	tgc	ctc	caa		1048
Val	Val	Ala	Val	Ala	Ile	Gly	Trp	Val	Cys	Arg	Asp	Arg	Cys	Leu	Gln		
			270				275					280					
cac	agc	tat	gca	ggc	gcc	tgg	gct	gtg	agt	ccg	gag	aca	gag	ctc	act		1096
His	Ser	Tyr	Ala	Gly	Ala	Trp	Ala	Val	Ser	Pro	Glu	Thr	Glu	Leu	Thr		
	285					290					295						
ggc	cac	gtt	tgaccgggagc	tcaccgcccc	gagcgtggac	agggcttccg											1145
Gly	His	Val															
300																	
tgagacgccca	ccgtgagagg	ccaggtggca	gcttgagcat	ggactcccag	actgcagggg												1205
agcacttggg	gcagccccca	gaaggaccac	tgctggatcc	cagggagaaac	ctgctggcgt												1265
tggtctgtgat	cctggaatga	ggcccttttc															1294
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Arg	Ala	Asp	Thr	Gln	Glu	Lys	Glu	Val	Arg	Ala	Met	Val	Gly	Ser	Asp		
			20					25					30				
Val	Glu	Leu	Ser	Cys	Ala	Cys	Pro	Glu	Gly	Ser	Arg	Phe	Asp	Leu	Asn		
		35					40					45					
Asp	Val	Tyr	Val	Tyr	Trp	Gln	Thr	Ser	Glu	Ser	Lys	Thr	Val	Val	Thr		
	50					55					60						
Tyr	His	Ile	Pro	Gln	Asn	Ser	Ser	Leu	Glu	Asn	Val	Asp	Ser	Arg	Tyr		
65					70					75					80		
Arg	Asn	Arg	Ala	Leu	Met	Ser	Pro	Ala	Gly	Met	Leu	Arg	Gly	Asp	Phe		
				85					90					95			
Ser	Leu	Arg	Leu	Phe	Asn	Val	Thr	Pro	Gln	Asp	Glu	Gln	Lys	Phe	His		
			100					105					110				

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

<210> 19

<211> 322

<212> PRT

<213> Mus musculus

0978420-0248260

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Leu	Phe	Leu 35	Leu	Leu	Leu	Ser	Ser 40	Leu	Cys	Ala	Ala	Ser 45	Ala	Glu	Thr
Glu	Val 50	Gly	Ala	Met	Val	Gly 55	Ser	Asn	Val	Val	Leu 60	Ser	Cys	Ile	Asp
Pro 65	His	Arg	Arg	His	Phe 70	Asn	Leu	Ser	Gly	Leu 75	Tyr	Val	Tyr	Trp	Gln 80
Ile	Glu	Asn	Pro	Glu 85	Val	Ser	Val	Thr	Tyr 90	Tyr	Leu	Pro	Tyr	Lys 95	Ser
Pro	Gly	Ile	Asn 100	Val	Asp	Ser	Ser	Tyr 105	Lys	Asn	Arg	Gly	His 110	Leu	Ser
Leu	Asp	Ser 115	Met	Lys	Gln	Gly	Asn 120	Phe	Ser	Leu	Tyr	Leu 125	Lys	Asn	Val
Thr	Pro 130	Gln	Asp	Thr	Gln	Glu 135	Phe	Thr	Cys	Arg	Val 140	Phe	Met	Asn	Thr
Ala 145	Thr	Glu	Leu	Val	Lys 150	Ile	Leu	Glu	Glu	Val 155	Val	Arg	Leu	Arg	Val 160
Ala	Ala	Asn	Phe	Ser 165	Thr	Pro	Val	Ile	Ser 170	Thr	Ser	Asp	Ser	Ser 175	Asn
Pro	Gly	Gln	Glu 180	Arg	Thr	Tyr	Thr	Cys 185	Met	Ser	Lys	Asn	Gly 190	Tyr	Pro
Glu	Pro	Asn 195	Leu	Tyr	Trp	Ile	Asn 200	Thr	Thr	Asp	Asn	Ser 205	Leu	Ile	Asp
Thr	Ala 210	Leu	Gln	Asn	Asn	Thr 215	Val	Tyr	Leu	Asn	Lys 220	Leu	Gly	Leu	Tyr
Asp 225	Val	Ile	Ser	Thr	Leu 230	Arg	Leu	Pro	Trp	Thr 235	Ser	Arg	Gly	Asp	Val 240
Leu	Cys	Cys	Val	Glu 245	Asn	Val	Ala	Leu	His 250	Gln	Asn	Ile	Thr	Ser 255	Ile
Ser	Gln	Ala	Glu 260	Ser	Phe	Thr	Gly	Asn 265	Asn	Thr	Lys	Asn	Pro 270	Gln	Glu
Thr	His	Asn 275	Asn	Glu	Leu	Lys	Val 280	Leu	Val	Pro	Val	Leu 285	Ala	Val	Leu
Ala	Ala 290	Ala	Ala	Phe	Val	Ser 295	Phe	Ile	Ile	Tyr	Arg 300	Arg	Thr	Arg	Pro
His 305	Arg	Ser	Tyr	Thr	Gly 310	Pro	Lys	Thr	Val	Gln 315	Leu	Glu	Leu	Thr	Asp 320

His Ala

<210> 20

<211> 143

<212> PRT

<213> Artificial sequence

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<221> misc_feature

<223> Synthetic

<400> 20

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1 5 10 15
Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr Val Tyr Trp
20 25 30
Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg Ser Met Gly
35 40 45
Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys Val Leu Val
50 55 60
Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr Thr Cys Ser
65 70 75 80
Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn Ser Leu Asp
85 90 95
Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val Ser Leu Arg
100 105 110
Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly Lys Lys Leu
115 120 125
Ala Val Leu Val Ile Arg Arg Ser Tyr Gly Val Glu Leu Thr His
130 135 140

<210> 21

<211> 1370

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

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<222> (1)..(165)

<220>

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<222> (166)..(762)

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tatagggaaa gctggtacgc ctgcaggtag cggtccggaa ttcccgggtc gaccacgcg 120
tccgtgaaca ctgaacgcga ggactgttaa ctgtttctgg caaac atg aag tca ggc 177
Met Lys Ser Gly
1
ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt tta aca gga 225
Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly
5 10 15 20
gaa atc aat ggt tct gcc aat tat gag atg ttt ata ttt cac aac gga 273
Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly
25 30 35
ggg gta caa att tta tgc aaa tat cct gac att gtc cag caa ttt aaa 321
Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
40 45 50
atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc act aag aca 369
Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
55 60 65
aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa ttc tgc cat 417
Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
70 75 80
tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac aac ttg gac 465
Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
85 90 95 100
cat tct cat gcc aac tat tac ttc tgc aac cta tca att ttt gat cct 513
His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
105 110 115
cct cct ttt aaa gta act ctt aca gga gga tat ttg cat att tat gaa 561
Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu
120 125 130
tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc ata gga tgt gca 609
Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala
135 140 145
gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt att tgt tgg ctt 657
Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu
150 155 160
aca aaa aag aag tat tca tcc agt gtg cac gac cct aac ggt gaa tac 705
Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr
165 170 175 180

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atg ttc atg aga gca gtg aac aca gcc aaa aaa tct aga ctc aca gat 753
Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp
185 190 195

gtg acc cta taatatggaa ctctggcacc caggcatgaa gcacgttggc 802
Val Thr Leu

cagttttcct caacttgaag tgcaagattc tcttatttcc gggaccacgg agagtctgac 862

ttaactacat acatcttctg ctggtgtttt gttcaatctg gaagaatgac tgtatcagtc 922

aatgggggatt ttaacagact gccttggtac tgccgagtc tctcaaaaca aacaccctct 982

tgcaaccagc tttggagaaa gccagctcc tgtgtgtctca ctgggagtg aatccctgtc 1042

tccacatctg ctcttagcag tgcacagccc agtaaaacaa acacatttac aagaaaaatg 1102

ttttaaagat gccaggggta ctgaatctgc aaagcaaag agcagccaag gaccagcatc 1162

tgctccgcatc tcactatcat actacctctt ctttctgtag ggatgagaat tcctctttta 1222

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<210> 22

<211> 199

<212> PRT

<213> Homo sapiens

<400> 22

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

Gln Gln Phe Lys Met Gln Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

09720420 "070204

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190

Arg Leu Thr Asp Val Thr Leu
195

<210> 23

<211> 199

<212> PRT

<213> Homo sapiens

<400> 23

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu

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115	120	125
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro		
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Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu		
145	150	155
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro		
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Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser		
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Arg Leu Thr Asp Val Thr Leu		
195		
<210> 24		
<211> 200		
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Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val		
35	40	45
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu		
50	55	60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro		
65	70	75
Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu		
85	90	95
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser		
100	105	110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr		
115	120	125
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu		
130	135	140
Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile		
145	150	155
Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp		
165	170	175
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys		
180	185	190

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Ser Arg Leu Ala Gly Val Thr Ser
195 200

<210> 25

<211> 24

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<223> Synthetic oglionucleotide

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24

<210> 26

<211> 23

<212> DNA

<213> Artificial sequence

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<223> Synthetic oglionucleotide

<400> 26
tgggtgaccta ccacatccca cag

23

<210> 27

<211> 23

<212> DNA

<213> Artificial sequence

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<221> misc_feature

<223> Synthetic oglionucleotide

097E420.070201

<400> 27
tccgatgtca tttcctgtct ggc

23

<210> 28

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<223> Synthetic oglionucleotide

<400> 28
gctctgtctc cggactcaca gccc

24

<210> 29

<211> 28

<212> DNA

<213> Artificial sequence

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<221> misc_feature

<223> Synthetic oglionucleotide

<400> 29
gtggcagcaa acttcagcgt gcccgtcg

28

<210> 30

<211> 28

<212> DNA

<213> Artificial sequence

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<221> misc_feature

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<223> Synthetic oglionucleotide

<400> 30
cccaacgtgt actggatcaa taagacgg 28

<210> 31

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<223> Synthetic oglionucleotide

<400> 31
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<210> 32

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<212> DNA

<213> Artificial sequence

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<223> Synthetic oglionucleotide

<400> 32
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<210> 33

<211> 21

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<220>

09733420-070201

<221> misc_feature
<223> Synthetic oglionucleotide

<400> 33
cgccgtgttc catttatgag c

21

<210> 34
<211> 18
<212> DNA
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<220>
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<223> Synthetic oglionucleotide

<400> 34
gcatatttat gaatccca

18

<210> 35
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<223> Synthetic oglionucleotide

<400> 35
actattaggg tcatgcac

18

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